Exhibit B

GUARDANT360®

Assay **Specifications**

About Guardant360

Guardant360 is a comprehensive liquid profiling test that evaluates 740 genes and includes TMB, MSI status, CHIP filtering, and methylation-based features.

Test Specifications

Sample input	Sample specifications	Turnaround time
Two 10 mL tubes of whole blood	Ship same or next day at room temperature - do not freeze or refrigerate	7 days from sample receipt to results*

Performance Specifications

Alterations	Limit of Detection at 95% Sensitivity†	Specificity	Threshold for Positivity‡
SNVs	0.20%	≥99.9%	≥0.001%
Indels	0.26%	≥99.9%	≥0.01%
CNAs	2.46 copies	≥99.9%	≥2.16 copies
Fusions/Rearrangements	0.15%	≥99.9%	≥2 unique molecules
MSI-High	0.05%	≥99.9%	—
Tumor Fraction	0.05%	—	—
TMB	≥0.3%§	—	—
Promoter Methylation	1.6%	—	≥5 methylated molecules

*Median turnaround time from sample receipt to results.
†Limit of detection (LoD) defined as the allele fraction/copy number at which the test has a 95% probability of detection for oncogenic variants and genes with relevance in guidelines, drug labels, and clinical trials.
‡Indicates mutant allele fraction for detected SNVs and Indels.
§Tumor mutation burden (TMB) evaluable at or above a sample allele fraction of 0.3%.
CHIP: Clonal Hematopoiesis of Indeterminate Potential; CNA: Copy Number Amplification; MSI: Microsatellite Instability; SNV: Single Nucleotide Variant.

Important Note: The Guardant360 test was developed as a Laboratory Developed Test (LDT), and its performance characteristics determined, by the Guardant Health Clinical Laboratory in Redwood City, CA, USA, which is certified under the Clinical Laboratory Improvement Amendments of 1988 (CLIA) as qualified to perform high-complexity testing. This test has not been cleared or approved by the US FDA.

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Assay **Specifications**

Gene Panel

MSI status - Qualitative result

TMB - Mutations per megabase

CHIP - Potential variants noted

Tumor fraction - Percent

ABCB1
ABL1
ABL2
ABRAXAS1
ACVR1
ACVR1B
ACVR2A
ADARB2
ADGRA2
ADGRG4
AFDN
AGGF1
AIP
AKT1
AKT1S1
AKT2
AKT3
ALB
ALK‖
ALOX12B
ALOX15B
ALOX5
AMER1
APC††
APEX1
APLNR
AR#
ARAF
ARFRP1
ARHGAP35
ARID1A††
ARID1B††
ARID2
ASXL1
ATM‖**††
ATMIN
ATR††
ATRX
AURKA
AURKB
AURKC
AXIN1
AXIN2
AXL
B2M††
BABAM1
BABAM2
BAP1
BARD1
BCL2
BCL2L1
BCL2L2
BCL6
BCOR
BCORL1
BCR
BIRC5
BLM
BMPR1A
BRAF#‖
BRCA1‖**††
BRCA2‖**††
BRCC3
BRD2
BRD3
BRD4
BRIP1††
BSG
BTG1
BTG2
BTK
BUB1B
C9orf78
CALR
CARD11
CASP8
CASR
CAV1
CBFB
CBL
CBLB
CCAR1
CCN6
CCNA2
CCNB1
CCND1#
CCND2#
CCND3
CCNE1#
CCNE2
CD274
CD276
CD74
CD79A
CD79B
CDC27
CDC5L
CDC7
CDC73
CDH1††
CDH6
CDK11A
CDK12‖**††
CDK4#
CDK6#
CDK7
CDK8
CDKN1A
CDKN1B††
CDKN1C
CDKN2A‖**††
CDKN2B
CDKN2C
CEBPA
CELF4
CEP295
CFAP20
CHD4
CHEK1††
CHEK2‖**††
CIC
CMTM4
CMTM6
CNOT3
CREBBP
CRKL
CRTC1
CSF1R
CSF3R
CTC1
CTCF
CTLA4
CTNNA1
CTNNB1
CUL3
CUL4A
CUX1
CWC22
CXCR4
CYLD
CYP17A1
CYP19A1
CYP2C19
CYP3A4
DAXX
DCUN1D1
DDIT3
DDR1
DDR2
DDX17
DDX18
DDX27
DDX3X
DDX41
DEPDC5
DEPTOR
DHX15
DHX16
DHX36
DHX9
DICER1
DIS3L2
DLL4
DNAJB1
DNMT1
DNMT3A
DNMT3B
DOT1L
DPYD
DUSP4
DYNLL1
DYRK2
E2F3
ECT2L
EFTUD2
EGFR#‖
EIF1AX
EIF4A1
EIF4A2
EIF4A3
EIF4B
EIF4E
EIF4E2
ELAVL1
ELAVL2
ELF3
ELOC
EML4
EMSY
EP300
EPCAM
EPHA3
EPHA5
EPHA7
EPHB1
ERBB2# (HER2)
ERBB3
ERBB4
ERCC1
ERCC2
ERCC3
ERCC4
ERCC5
ERCC6
ERCC6L2
ERCC8
EREG
ERF
ERG
ERRFI1
ESR1#‖
ETS1
ETV1
ETV4
ETV5
ETV6
EWSR1
EXO1
EZH1
EZH2
FAAP100
FAAP20
FAAP24
FANCA††
FANCB
FANCC
FANCD2
FANCE††
FANCF††
FANCG††
FANCI
FANCL††
FANCM
FAS
FAT1
FBXW7
FCGR2A
FCGR3A
FEN1
FGF1
FGF10
FGF12
FGF14
FGF19
FGF2
FGF23
FGF3
FGF4
FGF5
FGF6
FGF7
FGF8
FGF9
FGFR1#‖
FGFR2#‖
FGFR3‖
FGFR4
FH
FLCN
FLT1
FLT3
FLT4
FOXA1
FOXL2
FOXO1
FOXP1
FRS2
FUBP1
FUBP3
FUS
FYN
FZD1
FZD10
FZD2
FZD3
FZD4
FZD5
FZD6
FZD7
FZD8
FZD9
GAS6
GATA1
GATA2
GATA3
GATA4
GATA6
GEN1
GID4
GLI1
GNA11
GNA13
GNAQ
GNAS
GPATCH8
GPC3
GREM1
GRIN2A
GSK3B
GSTM1
GSTP1
H3-4
H3F3A
HACD4
HDAC2
HDAC6
HELQ
HES1
HEY1
HEYL
HGF
HNF1A
HNRNPDL
HOXB13
HRAS
HSD3B1
HSP90AA1
ICOSLG
ID3
IDH1
IDH2
IDO1
IFNG
IFNGR1
IFNGR2
IFNW1
IGF1
IGF1R
IGF2
IGF2BP3
IGF2R
IKBKE
IKZF1
IL1R1
IL2RA
IL2RB
IL2RG
IL7R
INHBA
INPP4B
INTS6L
IRF1
IRF2
IRF4
IRS2
JAK1
JAK2
JAK3
JUN
KAT6A
KAT6B
KDM4A
KDM5A
KDM5B
KDM5C
KDM6A
KDR
KEAP1‖**††
KIN
KIT#
KLF4
KLHL6
KLHL9
KMT2A
KMT2B
KMT2C
KMT2D
KNSTRN
KRAS#
LATS1
LGR4
LGR5
LGR6
LIG1
LIG4
LMO1
LRP1B
LRP2
LRP5
LRP6
LTK
LYN
LZTR1
MAD2L2
MALT1
MAP2K1
MAP2K2
MAP2K4
MAP3K1
MAP3K13
MAP4K3
MAPK1
MAPK3
MAPKAP1
MARK2
MAX
MCL1
MDC1
MDM2
MDM4
MED12
MEF2B
MEN1
MERTK
MET‖#
MGA
MGMT‡‡
MITF
MKNK1
MLH1††
MLH3
MLST8
MPL
MRAS
MRE11
MSH2††
MSH3
MSH6††
MTAP‖**††
MTHFR
MTOR
MUTYH††
MYB
MYC#
MYCL
MYCN
MYD88
MYOD1
NAB2
NBN
NCOR1
NCR1
NCR3
NEGR1
NELFE
NF1††
NF2††
NFE2L2
NFKBIA
NHEJ1
NKX2-1
NOTCH1
NOTCH2
NOTCH3
NOTCH4
NOVA1
NPM1
NPRL2
NPRL3
NRAS
NRG1‖
NSD1
NSD2
NSD3
NSRP1
NTHL1
NTRK1‖
NTRK2‖
NTRK3‖
NUMA1
NUMB
NUP93
NUTM1
P2RY8
PABPC1
PAK1
PAK3
PALB2‖**††
PARG
PARP1
PARP2
PAX3
PAX5
PAX7
PAX8
PAXIP1
PBRM1††
PCBP1
PCBP2
PCDH15
PDCD1
PDCD1LG2
PDE7A
PDGFRA#
PDGFRB
PDK1
PDPK1
PHF6
PHLPP1
PHLPP2
PHOX2B
PIAS4
PIK3C2B
PIK3CA#
PIK3CB
PIK3CD
PIK3CG
PIK3R1
PIK3R2
PIK3R3
PIM1
PIN1
PKM
PLCG2
PLEKHS1
PLRG1
PMS1
PMS2††
POLA1
POLD1
POLE††
POLH
POLQ
POT1
POU2F2
PPARG
PPIG
PPM1D
PPP2CA
PPP2R1A
PPP2R2A
PPP3CA
PPP6C
PRDM1
PREX1
PREX2
PRKAR1A
PRKCI
PRKDC
PRKN
PRMT5
PRPF40B
PRPF4B
PSENEN
PSMB10
PSMB8
PSMB9
PTCH1
PTDSS1
PTEN‖**††
PTPN11
PTPN2
PTPRD
PTPRS
PTPRT
QKI
RAB35
RAC1
RAD18
RAD21
RAD50††
RAD51††
RAD51B
RAD51C‖**††
RAD51D‖**††
RAD52
RAD54L
RAET1E
RAF1#
RARA
RASA1
RB1‖**††
RBBP6
RBM10
RBMX
RECQL
RECQL4
RET‖
REV3L
RGS1
RHEB
RHOA
RHOB
RICTOR
RIF1
RILPL1
RIT1
RNASEH2B
RNF43
ROBO1
ROBO2
ROS1‖
RPA1
RPS27A
RPS6KA3
RPS6KB1
RPS6KB2
RPTOR
RRAGC
RSPO1
RSPO2
RSPO4
RUNX1
RUNX1T1
RXRA
RYBP
SAMHD1
SDC4
SDHA††
SDHAF2
SDHB††
SDHC††
SDHD††
SEM1
SERPINB3
SERPINB4
SESN2
SETD2
SF3B1
SF3B3
SH2D1A
SHLD1
SHLD2
SLC34A2
SLFN11
SLIT2
SMAD2
SMAD3
SMAD4††
SMARCA2
SMARCA4
SMARCAL1
SMARCB1
SMARCD1
SMARCE1
SMC1A
SMC3
SMO
SNCAIP
SOCS1
SOCS3
SOS1
SOX10
SOX17
SOX2
SOX9
SPEN
SPOP
SRC
SRSF2
SRY
SS18
STAG2
STAT1
STAT3
STAT4
STK11‖**††
STK19
STK40
STN1
SUFU
SYK
SYNCRIP
TACSTD2 (TROP2)
TAF1L
TAP1
TAP2
TAPBP
TBC1D7
TBX3
TCERG1
TCF7L2
TEK
TEN1
TENT5C
TERT¶
TET1
TET2
TFE3
TFRC
TGFBR1
TGFBR2
THRAP3
TIA1
TIPARP
TMEM127
TMPRSS2
TNFAIP3
TNFRSF14
TNFRSF1A
TNK2
TNPO1
TOP1
TOP2A
TOPAZ1
TP53††
TP53BP1
TP63
TP73
TPMT
TRAF2
TRAF3
TRAF7
TRIM24
TRIP13
TSC1
TSC2††
TSHR
TSHZ2
TYMP
TYMS
TYRO3
U2AF1
UBE2T
UGT1A1
UIMC1
ULBP1
ULBP3
USP28
USP7
USP9X
VEGFA
VEGFB
VHL
VIRMA
WBP11
WEE1
WRN
WT1
WWP1
XBP1
XPA
XPC
XPO1
XRCC1
XRCC2
XRCC3
XRCC4
XRCC5
XRCC6
YAP1
YES1
ZC3H13
ZC3H18
ZC3H4
ZMYM3
ZNF217
ZNF703
ZNRF3
ZRSR2

¶Includes *TERT* promoter region. #Includes CNAs. ‖Includes Fusions/Rearrangements. **Includes Copy Number Losses. ††Includes Promoter Methylation. ‡‡Promoter Methylation only.

CHIP filter is based on a proprietary algorithm that identifies variants that are potentially derived from clonal hematopoiesis.

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